

RAW SEQUENCE LISTING

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Application Serial Number: 10/659,755B
Source: IFW/6
Date Processed by STIC: 04/09/2007

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/659,755B

DATE: 04/09/2007

TIME: 15:00:08

Input Set : N:\EFS\04_09_07\10659755B_efs\NBLE007US.txt
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3 <110> APPLICANT: DIXON, RICHARD A.
 4 LIU, CHANG-JUN
 5 DEAVOURS, BETTINA
 7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
 8 AND ISOFLAVONOID NUTRACEUTICALS
 10 <130> FILE REFERENCE: NBLE:007US
 12 <140> CURRENT APPLICATION NUMBER: 10/659,755B
 13 <141> CURRENT FILING DATE: 2003-09-10
 15 <150> PRIOR APPLICATION NUMBER: 60/409,447
 16 <151> PRIOR FILING DATE: 2002-09-10
 18 <160> NUMBER OF SEQ ID NOS: 15
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1824
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Soybean
 27 <400> SEQUENCE: 1
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 29 ttgaacttgc acttggttta ttgggtttgg ctctgtttct gcacttgcgt cccacaccca 120
 30 ctgcacaaatc aaaagcactt cgccatctcc caaaccacc aagcccaaag cctcgtcttc 180
 31 ccttcatagg acaccttcat ctcttaaaag acaaacttct ccactacgca ctcatcgacc 240
 32 tctccaaaaaa acatggtccc ttattctctc tctactttgg ctccatgcca accgttgg 300
 33 cctccacacc agaattgttc aagctctcc tccaaacgca cgaggcaact tccttcaaca 360
 34 caaggttcca aacctcagcc ataagacgccc tcacccatgaa tagctcagtg gccatgg 420
 35 cttcggacc ttactgaaag ttcgtgagga agctcatcat gaacgacctt cccaaacgcca 480
 36 ccactgtaaa caagttgagg ccttggagg cccaaacagac ccgcaagtcc cttagggtt 540
 37 tggcccaagg cgcagaggca cagaagcccc ttgacttgac cgaggagctt ctgaaatgga 600
 38 ccaacagcac catctccatg atgatgctcg gcgaggctga ggagatcaga gacatcgctc 660
 39 gcgaggttct taagatcttt ggcgaataaca gcctcaactga cttcatctgg ccattgaagc 720
 40 atctcaaggat tggaaagtat gagaagagga tcgacgacat cttgaacaag ttcgaccctg 780
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 45 atctcaaggat gttggaaaag gctcgtgagg aggtctacag ttgttgggaa aaggacagac 1080
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 47 tccgcattgc cccgcactc ccagtggtca aaagaaagtg cacagaagag tgtgagatta 1200
 48 atgatatgt gatcccagag ggagcattga ttctttcaa tgtatggcaa gttagaagag 1260
 49 accccaaata ctgggacaga ccatcgagg tccgtctga gaggttccctt gagacagggg 1320
 50 ctgaaggggaa agcaggccctt ctgtatctta ggggacaaca ttttcaactt ctcccatctt 1380
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 53 agggttgta cgccaaagtt agcatgaaag agagagccgg cctcaactt ccaagggcac 1560

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54 atagtcttgt ctgtgttcca cttgcaagga tcggcggtgc atctaaactc ctttcttaat 1620
 55 taagatcatc atcatatata atatttactt tttgtgtgtt gataatcatc atttcaataa 1680
 56 ggtctcggttc atctactttt tatgaagtat ataaggccctt ccatgcacat tgtatcatct 1740
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 58 actataaaact atcaatcctt atat 1824
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 63 <212> TYPE: PRT
 64 <213> ORGANISM: Soybean
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 68 1 5 10 15
 70 His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
 71 20 25 30
 73 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
 74 35 40 45
 76 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
 77 50 55 60
 79 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
 80 65 70 75 80
 82 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
 83 85 90 95
 85 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
 86 100 105 110
 88 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
 89 115 120 125
 91 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Pro Asn Ala Thr Thr
 92 130 135 140
 94 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
 95 145 150 155 160
 97 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
 98 165 170 175
 100 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 101 180 185 190
 103 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 104 195 200 205
 106 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
 107 210 215 220
 109 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 110 225 230 235 240
 112 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 113 245 250 255
 115 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
 116 260 265 270
 118 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
 119 275 280 285
 121 Ile Thr Lys Asp His Ile Glu Gly Leu Val Val Asp Phe Phe Ser Ala
 122 290 295 300
 124 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu

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128	325	330	335	
130	Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu			
131	340	345	350	
133	Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro			
134	355	360	365	
136	Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly			
137	370	375	380	
139	Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val			
140	385	390	395	400
142	Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu			
143	405	410	415	
145	Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu			
146	420	425	430	
148	Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met			
149	435	440	445	
151	Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala			
152	450	455	460	
154	Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln			
155	465	470	475	480
157	Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly			
158	485	490	495	
160	Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg			
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168	<211> LENGTH: 950			
169	<212> TYPE: DNA			
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173	<221> NAME/KEY: CDS			
174	<222> LOCATION: (41)..(709)			
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181	acc gca atc act gtg gag aac ctt gaa tac cca gcg gtg gtt acc tct	103		
182	Thr Ala Ile Thr Val Glu Asn Leu Glu Tyr Pro Ala Val Val Thr Ser			
183	10	15	20	
185	ccg gtc acc ggc aaa tca tat ttc ctc ggt ggc gct ggg gag aga gga	151		
186	Pro Val Thr Gly Lys Ser Tyr Phe Leu Gly Gly Ala Gly Glu Arg Gly			
187	25	30	35	
189	ttg acc att gaa gga aac ttc atc aag ttc act gcc ata ggt gtt tat	199		
190	Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr Ala Ile Gly Val Tyr			
191	40	45	50	
193	ttg gaa gat ata gca gtg gct tca cta gct gcc aaa tgg aag ggt aaa	247		
194	Leu Glu Asp Ile Ala Val Ala Ser Leu Ala Lys Trp Lys Gly Lys			

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198	Ser	Ser	Glu	Glu	Leu	Leu	Glu	Thr	Leu	Asp	Phe	Tyr	Arg	Asp	Ile	Ile		
199	70				75				80							85		
201	tca	ggt	ccc	ttt	gaa	aag	tta	att	aga	ggg	tca	aag	att	agg	gaa	ttg	343	
202	Ser	Gly	Pro	Phe	Glu	Lys	Leu	Ile	Arg	Gly	Ser	Lys	Ile	Arg	Glu	Leu		
203					90				95							100		
205	agt	ggt	cct	gag	tac	tca	agg	aag	gtt	atg	gag	aac	tgt	gtg	gca	cac	391	
206	Ser	Gly	Pro	Glu	Tyr	Ser	Arg	Lys	Val	Met	Glu	Asn	Cys	Val	Ala	His		
207					105				110							115		
209	ttg	aaa	tca	gtt	gga	act	tat	gga	gat	gca	gaa	gct	gaa	gct	atg	caa	439	
210	Leu	Lys	Ser	Val	Gly	Thr	Tyr	Gly	Asp	Ala	Glu	Ala	Glu	Ala	Met	Gln		
211					120				125							130		
213	aaa	ttt	gtc	gaa	gct	ttc	aag	cct	gtt	aat	ttt	cca	cct	ggc	tct		487	
214	Lys	Phe	Ala	Glu	Ala	Phe	Lys	Pro	Val	Asn	Phe	Pro	Pro	Gly	Ala	Ser		
215					135				140							145		
217	gtt	ttc	tac	agg	caa	tca	cct	gat	gga	ata	tta	ggg	ctt	agt	ttc	tct	535	
218	Val	Phe	Tyr	Arg	Gln	Ser	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Ser	Phe	Ser		
219	150				155				160							165		
221	ccg	gat	aca	agt	ata	cca	gaa	aag	gag	gct	gca	ctc	ata	gag	aac	aag	583	
222	Pro	Asp	Thr	Ser	Ile	Pro	Glu	Lys	Glu	Ala	Ala	Leu	Ile	Glu	Asn	Lys		
223					170				175							180		
225	gca	gtt	tca	tca	gca	gtg	ttg	gag	act	atg	atc	ggc	gag	cac	gct	gtt	631	
226	Ala	Val	Ser	Ala	Val	Leu	Glu	Thr	Met	Ile	Gly	Glu	His	Ala	Val			
227					185				190							195		
229	tcc	cct	gat	ctt	aag	cgc	tgt	tta	gct	gca	aga	tta	cct	gcg	ttg	ttg	679	
230	Ser	Pro	Asp	Leu	Lys	Arg	Cys	Leu	Ala	Ala	Arg	Leu	Pro	Ala	Leu	Leu		
231					200				205							210		
233	aac	gag	ggt	gct	ttc	aag	att	gga	aac	tga	tgatgattat	actcctatat					729	
234	Asn	Glu	Gly	Ala	Phe	Lys	Ile	Gly	Asn									
235					215				220									
237	cactgcattt	ccaaaagcgt	tgcagcaca	aat	gagacc	atgaactttt	ttaagtctac										789	
239	acgtttaatt	ttttgtat	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	849
241	gtatctgctt	tctactctt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	909
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257					35				40							45		
258	Ala	Ile	Gly	Val	Tyr	Leu	Glu	Asp	Ile	Ala	Val	Ala	Ser	Leu	Ala	Ala		
259					50				55							60		
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261 65 70 75 80
 262 Tyr Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser
 263 85 90 95
 264 Lys Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Met Glu
 265 100 105 110
 266 Asn Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu
 267 115 120 125
 268 Ala Glu Ala Met Gln Lys Phe Ala Glu Ala Phe Lys Pro Val Asn Phe
 269 130 135 140
 270 Pro Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu
 271 145 150 155 160
 272 Gly Leu Ser Phe Ser Pro Asp Thr Ser Ile Pro Glu Lys Glu Ala Ala
 273 165 170 175
 274 Leu Ile Glu Asn Lys Ala Val Ser Ser Ala Val Leu Glu Thr Met Ile
 275 180 185 190
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 291 atggaaagggt aaatcatctg aagagttact tgagaccctt gacttttaca gagacatcat 180
 292 ctcaggtccc tttaaaaagt taatttagagg gtcaaagatt agggaaattga gtggccctga 240
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 301 tagtatgaaa tgaaaatct tgctttctac tcttgacta ttctgtgat agataatgtt 780
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 317 accaag atg gtg agt gta tct gaa att cgc aag gct cag agg gca gaa 108
 318 Met Val Ser Val Ser Glu Ile Arg Lys Ala Gln Arg Ala Glu

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